

Qy 1384 AGTGGAGATGAAGATGGAGAAGATCCAGACAAGAGAATTTCTATTTCGAGCATCAGACAAG 1443
 |||
 Db 462 SerGlyAspGluAspGlyGluAspProAspLysArgIleSerIleArgAlaSerAspLys 481

Qy 1444 CGGATAGCTTGTGATGAAGAATTCTCAGATTCTGAGGATGAAGGAGAGGAGGTCTGAAGA 1503
 |||
 Db 482 ArgIleAlaCysAspGluGluPheSerAspSerGluAspGluGlyGluGlyGlyArgArg 501

Qy 1504 AATGTGGCTGATCATAAGAAAGGAGCAAGAAAGCTAGAATTGAAGAAGATAAGAAAGAA 1563
 |||
 Db 502 AsnValAlaAspHisLysLysGlyAlaLysLysAlaArgIleGluGluAspLysLysGlu 521

Qy 1564 ACAGAGGACAAAAAACAGACGTTAAGGAAGAAGATAAATCCAAGGACAACAGTGGTGAA 1623
 |||
 Db 522 ThrGluAspLysLysThrAspValLysGluGluAspLysSerLysAspAsnSerGlyGlu 541

Qy 1624 AAAACAGATACCAAAGGAACCAATCAGAACAGCTCAGCAACCCC 1668
 |||
 Db 542 LysThrAspThrLysGlyThrLysSerGluGlnLeuSerAsnPro 556

RESULT 2

AAB49955

ID AAB49955 standard; protein; 488 AA.

XX

AC AAB49955;

XX

DT 08-MAR-2001 (first entry)

XX

DE Human histone deacetylase HDAC-2.

XX

KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy.

XX

OS Homo sapiens.

XX

PN WO200071703-A2.

XX

PD 30-NOV-2000.

XX

PF 03-MAY-2000; 2000WO-IB001252.

XX

PR 03-MAY-1999; 99US-0132287P.

XX

PA (METH-) METHYLGENE INC.

XX

PI Macleod AR, Li Z, Besterman JM;

XX

DR WPI; 2001-016407/02.

DR

N-PSDB; AAC89555.

XX

PT Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX

PS Disclosure; Page 51-53; 125pp; English.

XX

CC The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified

CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia

XX

SQ Sequence 488 AA;

Alignment Scores:

Pred. No.:	4.1e-248	Length:	488
Score:	2636.00	Matches:	488
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	74.5%	Indels:	0
DB:	4	Gaps:	0

US-10-528-104-5 (1-1985) x AAB49955 (1-488)

Qy	205	ATGGCGTACAGTCAAGGAGGCGGCAAAAAAAAAAGTCTGCTACTACTACGACGGTGATATT	264
Db	1	MetAlaTyrSerGlnGlyGlyGlyLysLysLysValCysTyrTyrTyrAspGlyAspIle	20
Qy	265	GGAAATTATTATTATGGACAGGGTCATCCCATGAAGCCTCATAGAATCCGCATGACCCAT	324
Db	21	GlyAsnTyrTyrTyrGlyGlnGlyHisProMetLysProHisArgIleArgMetThrHis	40
Qy	325	AACTTGCTGTAAATTATGGCTTATACAGAAAAATGGAAATATATAGGCCCCATAAAGCC	384
Db	41	AsnLeuLeuLeuAsnTyrGlyLeuTyrArgLysMetGluIleTyrArgProHisLysAla	60
Qy	385	ACTGCCGAAGAAATGACAAAATATCACAGTGATGAGTATATCAAATTTCTACGGTCAATA	444
Db	61	ThrAlaGluGluMetThrLysTyrHisSerAspGluTyrIleLysPheLeuArgSerIle	80
Qy	445	AGACCAGATAACATGTCTGAGTATAGTAAGCAGATGCATATATTTAATGTTGGAGAAGAT	504
Db	81	ArgProAspAsnMetSerGluTyrSerLysGlnMetHisIlePheAsnValGlyGluAsp	100
Qy	505	TGTCCAGCGTTTGATGGACTCTTTGAGTTTTGTCAGCTCTCAACTGGCGGTTTCAGTTGCT	564
Db	101	CysProAlaPheAspGlyLeuPheGluPheCysGlnLeuSerThrGlyGlySerValAla	120
Qy	565	GGAGCTGTGAAGTTAAACCGACAACAGACTGATATGGCTGTTAATTGGGCTGGAGGATTA	624
Db	121	GlyAlaValLysLeuAsnArgGlnGlnThrAspMetAlaValAsnTrpAlaGlyGlyLeu	140
Qy	625	CATCATGCTAAGAAATACGAAGCATCAGGATTCTGTTACGTTAATGATATTGTGCTTGCC	684
Db	141	HisHisAlaLysLysTyrGluAlaSerGlyPheCysTyrValAsnAspIleValLeuAla	160
Qy	685	ATCCTTGAATTACTAAAGTATCATCAGAGAGTCTTATATATTGATATAGATATTCATCAT	744
Db	161	IleLeuGluLeuLeuLysTyrHisGlnArgValLeuTyrIleAspIleAspIleHisHis	180
Qy	745	GGTGATGGTGTGAAGAAGCTTTTTATACAACAGATCGTGTAAATGACGGTATCATTCCAT	804
Db	181	GlyAspGlyValGluGluAlaPheTyrThrThrAspArgValMetThrValSerPheHis	200
Qy	805	AAATATGGGGAATACTTTCTGGCACAGGAGACTTGAGGGATATTGGTGCTGGAAAAGGC	864
Db	201	LysTyrGlyGluTyrPheProGlyThrGlyAspLeuArgAspIleGlyAlaGlyLysGly	220
Qy	865	AAATACTATGCTGTCAATTTTCCAATGTGTGATGGTATAGATGATGAGTCATATGGGCAG	924

Db	221	 LysTyrTyrAlaValAsnPheProMetCysAspGlyIleAspAspGluSerTyrGlyGln	240
Qy	925	ATATTTAAGCCTATTATCTCAAAGGTGATGGAGATGTATCAACCTAGTGCTGTGGTATTA	984
Db	241	 IlePheLysProIleIleSerLysValMetGluMetTyrGlnProSerAlaValValLeu	260
Qy	985	CAGTGTGGTGCAGACTCATTATCTGGTGATAGACTGGGTTGTTTCAATCTAACAGTCAAA	1044
Db	261	 GlnCysGlyAlaAspSerLeuSerGlyAspArgLeuGlyCysPheAsnLeuThrValLys	280
Qy	1045	GGTCATGCTAAATGTGTAGAAGTTGTAAAACTTTTAACTTACCATTACTGATGCTTGGA	1104
Db	281	 GlyHisAlaLysCysValGluValValLysThrPheAsnLeuProLeuLeuMetLeuGly	300
Qy	1105	GGAGGTGGCTACACAATCCGTAATGTTGCTCGATGTTGGACATATGAGACTGCAGTTGCC	1164
Db	301	 GlyGlyGlyTyrThrIleArgAsnValAlaArgCysTrpThrTyrGluThrAlaValAla	320
Qy	1165	CTTGATTGTGAGATTCCCAATGAGTTGCCATATAATGATTACTTTGAGTATTTTGGACCA	1224
Db	321	 LeuAspCysGluIleProAsnGluLeuProTyrAsnAspTyrPheGluTyrPheGlyPro	340
Qy	1225	GACTTCAAACATGCATATTAGTCCTTCAAACATGACAAACCAGAACACTCCAGAATATATG	1284
Db	341	 AspPheLysLeuHisIleSerProSerAsnMetThrAsnGlnAsnThrProGluTyrMet	360
Qy	1285	GAAAAGATAAAACAGCGTTTGTGTTGAAAATTTGCGCATGTTACCTCATGCACCTGGTGTC	1344
Db	361	 GluLysIleLysGlnArgLeuPheGluAsnLeuArgMetLeuProHisAlaProGlyVal	380
Qy	1345	CAGATGCAAGCTATTCCAGAAGATGCTGTTTCATGAAGACAGTGGAGATGAAGATGGAGAA	1404
Db	381	 GlnMetGlnAlaIleProGluAspAlaValHisGluAspSerGlyAspGluAspGlyGlu	400
Qy	1405	GATCCAGACAAGAGAATTTCTATTTCGAGCATCAGACAAGCGGATAGCTTGTGATGAAGAA	1464
Db	401	 AspProAspLysArgIleSerIleArgAlaSerAspLysArgIleAlaCysAspGluGlu	420
Qy	1465	TTCTCAGATTCTGAGGATGAAGGAGAAGGAGGTCGAAGAAATGTGGCTGATCATAAGAAA	1524
Db	421	 PheSerAspSerGluAspGluGlyGluGlyGlyArgArgAsnValAlaAspHisLysLys	440
Qy	1525	GGAGCAAAGAAAGCTAGAATTGAAGAAGATAAGAAAGAAACAGAGGACAAAAAACAGAC	1584
Db	441	 GlyAlaLysLysAlaArgIleGluGluAspLysLysGluThrGluAspLysLysThrAsp	460
Qy	1585	GTTAAGGAAGAAGATAAATCCAAGGACAACAGTGGTGAAAAACAGATACCAAAGGAACC	1644
Db	461	 ValLysGluGluAspLysSerLysAspAsnSerGlyGluLysThrAspThrLysGlyThr	480
Qy	1645	AAATCAGAACAGCTCAGCAACCCC	1668
Db	481	 LysSerGluGlnLeuSerAsnPro	488

RESULT 3

ABR47485

ID ABR47485 standard; protein; 488 AA.

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AC ABR47485;

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